

086,002 - SeqList.ST25.txt  
SEQUENCE LISTING

<110> Geron Corporation  
Majumdar, Anish Sen  
Ferber, Iris  
Frolkis, Maria  
Wang, Zhuo

<120> Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase Reverse Transcriptase

<130> 086/002

<140> [to be assigned]

<141> 2003-06-24

<150> 60/393,295

<151> 2002-06-27

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 4015

<212> DNA

<213> Homo sapiens

<400> 1

```
gcagcgctgc gtcctgctgc gcacgtggga agccctggcc ccggccaccc ccgcgatgcc      60
gcgcgctccc cgctgccgag ccgtgcgctc cctgctgcgc agccactacc gcgaggtgct      120
gccgctggcc acgttcgtgc ggcgcctggg gccccagggc tggcggctgg tgcagcgcg      180
ggacccggcg gctttccgcg cgctggtggc ccagtgcctg gtgtgcgtgc cctgggacgc      240
acggccgccc ccgcccgc ctccttccg ccaggtgtcc tgctgaagg agctggtggc      300
ccgagtgctg cagaggctgt gcgagcgcg cgcaagaac gtgctggcct tcggcttcgc      360
gctgctggac ggggcccgcg ggggcccc cagggccttc accaccagcg tgcgcagcta      420
cctgcccac acggtgaccg acgcactgcg ggggagcggg gcgtgggggc tgctgctgcg      480
ccgcgtgggc gacgacgtgc tggttcacct gctggcacgc tgcgcgctct ttgtgctggt      540
ggctcccagc tgcgcctacc aggtgtgcgg gccgccgctg taccagctcg gcgctgccac      600
tcaggcccg ccccgccac acgctagtgg accccgaagg cgtctgggat gcgaacgggc      660
ctggaaccat agcgtcaggg aggccggggt ccccctgggc ctgccagccc cgggtgag      720
gaggcgcggg ggcagtgcc gccgaagtct gccgttgccc aagaggccca ggcgtggcgc      780
tgcccctgag ccggagcgga cgcccgttg gcagggtcc tggggccacc cgggcaggac      840
gcgtggaccg agtgaccgtg gtttctgtgt ggtgtcacct gccagaccg ccgaagaagc      900
cacctctttg gagggtgcgc tctctggcac gcgccactcc caccatccg tgggccgcca      960
gcaccacgcg ggcccccat ccacatcgcg gccaccacgt ccctgggaca cgccttgctc     1020
```

## 086,002 - SeqList.ST25.txt

cccgggtgtac gccgagacca agcacttcct ctactcctca ggcgacaagg agcagctgcg	1080
gccctccttc ctactcagct ctctgaggcc cagcctgact ggcgctcgga ggctcgtgga	1140
gaccatcttt ctgggttcca ggccctggat gccagggact ccccgaggt tgccccgcct	1200
gccccagcgc tactggcaaa tgcggcccct gtttctggag ctgcttgga accacgcgca	1260
gtgcccctac ggggtgctcc tcaagacgca ctgcccgtg cgagctgcgg tcaccccagc	1320
agccgggtgtc tgtgcccggg agaagcccca gggctctgtg gcggcccccg aggaggagga	1380
cacagacccc cgtcgcctgg tgcagctgct ccgccagcac agcagcccct ggcaggtgta	1440
cggttcgtg cgggcctgcc tgcgccggct ggtgccccca ggcctctggg gctccaggca	1500
caacgaacgc cgcttcctca ggaacaccaa gaagttcatc tccctgggga agcatgccaa	1560
gctctcgctg caggagctga cgtggaagat gagcgtgcgg gactgcgctt ggctgcgcag	1620
gagcccaggg gttggctgtg ttccggccgc agagcaccgt ctgctgagg agatcctggc	1680
caagttcctg cactggctga tgagtgtgta cgtcgtcag ctgctcaggt ctttctttta	1740
tgtcacggag accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag	1800
caagttgcaa agcattggaa tcagacagca cttgaagagg gtgcagctgc gggagctgtc	1860
ggaagcagag gtcaggcagc atcgggaagc caggcccgcc ctgctgacgt ccagactccg	1920
cttcatcccc aagcctgacg ggctgcggcc gattgtgaac atggactacg tcgtgggagc	1980
cagaacgttc cgcagagaaa agagggccga gcgtctcacc tcgaggggtga aggcactgtt	2040
cagcgtgctc aactacgagc gggcgcgggc cccggcctc ctgggcgcct ctgtgctggg	2100
cctggacgat atccacaggg cctggcgcac cttcgtgctg cgtgtgcggg cccaggaccc	2160
gccgcctgag ctgtactttg tcaaggtgga tgtgacgggc gcgtacgaca ccatcccca	2220
ggacaggctc acggagggtca tcgccagcat catcaaacc cagaacacgt actgcgtgcg	2280
tcggtatgcc gtggtccaga aggccgcca tgggcacgtc cgcaaggcct tcaagagcca	2340
cgtctctacc ttgacagacc tccagccgta catgcgacag ttcgtggctc acctgcagga	2400
gaccagcccc ctgagggatg ccgtcgtcat cgagcagagc tcctccctga atgaggccag	2460
cagtggcctc ttcgacgtct tcctacgctt catgtgccac cacgccgtgc gcatcagggg	2520
caagtcctac gtccagtgcc aggggatccc gcagggtcc atcctctcca cgctgctctg	2580
cagcctgtgc tacggcgaca tggagaacaa gctgtttgcg gggattcggc gggacgggct	2640
gctcctgcgt ttggtggatg atttcttggt ggtgacacct cacctaccc acgcgaaaac	2700
cttcctcagg acctgggtcc gaggtgtccc tgagtatggc tgcgtggtga acttgcgga	2760
gacagtgggtg aacttccctg tagaagacga ggccctgggt ggcacggctt ttgttcagat	2820
gccggccac ggcctattcc cctggtgcgg cctgctgctg gatacccgga ccctggaggt	2880
gcagagcgac tactccagct atgcccggac ctccatcaga gccagtctca cttcaaccg	2940

086,002 - SeqList.ST25.txt

cggcttcaag gctgggagga acatgcgtcg caaactcttt ggggtcttgc ggctgaagtg 3000  
 tcacagcctg tttctggatt tgcaggtgaa cagcctccag acggtgtgca ccaacatcta 3060  
 caagatcctc ctgctgcagg cgtacaggtt tcacgcatgt gtgctgcagc tcccatttca 3120  
 tcagcaagtt tggaagaacc ccacattttt cctgcgcgtc atctctgaca cggcctccct 3180  
 ctgctactcc atcctgaaag ccaagaacgc agggatgtcg ctgggggcca agggcgccgc 3240  
 cggccctctg cctccgagg ccgtgcagtg gctgtgccac caagcattcc tgctcaagct 3300  
 gactcgacac cgtgtcacct acgtgccact cctgggggtca ctcaggacag cccagacgca 3360  
 gctgagtcgg aagctcccg ggacgacgt gactgccctg gaggccgag ccaacccggc 3420  
 actgccctca gacttcaaga ccattcctgga ctgatggcca cccgcccaca gccaggccga 3480  
 gagcagacac cagcagccct gtcacgccgg gctctacgtc ccagggaggg aggggcggcc 3540  
 cacaccagg cccgcaccgc tgggagtctg aggcctgagt gagtgtttgg ccgaggcctg 3600  
 catgtccggc tgaaggctga gtgtccggct gaggcctgag cgagtgtcca gccaaaggct 3660  
 gagtgtccag cacacctgcc gtcttcactt cccacaggc tggcgctcgg ctccacccca 3720  
 gggccagctt ttcctacca ggagcccggc ttccactccc cacataggaa tagtccatcc 3780  
 ccagattcgc cattgttcac ccctcgcctt gccctccttt gccttcacc cccaccatcc 3840  
 aggtggagac cctgagaagg accctgggag ctctgggaat ttggagtga caaagggtgtg 3900  
 ccctgtacac aggcgaggac cctgcacctg gatgggggtc cctgtgggtc aaattggggg 3960  
 gaggtgctgt gggagtaaaa tactgaatat atgagttttt cagttttgaa aaaaa 4015

<210> 2  
 <211> 1132  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
65 70 75 80

086,002 - SeqList.ST25.txt

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly

325

330

335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575

086,002 - SeqList.ST25.txt

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg  
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile  
705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His  
740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp  
755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser  
770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu  
785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His  
805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro  
820 825 830

086,002 - SeqList.ST25.txt

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp  
835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu  
850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala  
865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys  
885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu  
900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe  
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser  
930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe  
945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly  
965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn  
980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln  
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln  
1010 1015 1020

Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp  
1025 1030 1035

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly  
1040 1045 1050

Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu  
1055 1060 1065

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr  
1070 1075 1080

086,002 - SeqList.ST25.txt

Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr  
1085 1090 1095

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr  
1100 1105 1110

Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys  
1115 1120 1125

Thr Ile Leu Asp  
1130

<210> 3  
<211> 3426  
<212> DNA  
<213> Mus musculus

<400> 3  
gtgggaggcc catcccggcc ttgagcacia tgaccgcgc tcctcgttgc cccgcggtgc 60  
gctctctgct gcgcagccga taccgggagg tgtggccgct ggcaaccttt gtgcggcgcc 120  
tggggcccga gggcaggcgg cttgtgcaac ccggggaccc gaagatctac cgcacttttg 180  
ttgcccaatg cctagtgtgc atgcaactggg gctcacagcc tccacctgcc gacctttcct 240  
tccaccaggt gtcatccctg aaagagctgg tggccagggt tgtgcagaga ctctgcgagc 300  
gcaacgagag aaacgtgctg gcttttggtc ttgagctgct taacgaggcc agaggcgggc 360  
ctcccatggc cttcactagt agcgtgcgta gctacttgcc caacactgtt attgagaccc 420  
tgcgtgtcag tgggtgcatgg atgctactgt tgagccgagt gggcgacgac ctgctggtct 480  
acctgctggc aactgtgctc ctttatcttc tgggtgcccc cagctgtgcc taccagggtgt 540  
gtgggtctcc cctgtaccaaa atttgtgcca ccacggatat ctggccctct gtgtccgcta 600  
gttacaggcc caccgcaccc gtgggcagga atttcactaa ccttaggttc ttacaacaga 660  
tcaagagcag tagtcgccag gaagcaccga aaccctggc cttgccatct cgagggtacaa 720  
agaggcatct gagtctcacc agtacaagtg tgccttcagc taagaaggcc agatgctatc 780  
ctgtcccag agtggaggag ggaccccaca ggcagggtgct accaacccca tcaggcaaat 840  
catgggtgcc aagtcctgct cgggtccccg aggtgcctac tgagagaaa gatttgtctt 900  
ctaaaggaaa ggtgtctgac ctgagtctct ctgggtcggg gtgctgtaaa cacaagccca 960  
gctccacatc tctgctgtca ccaccccgcc aaaatgcctt tcagctcagg ccattttattg 1020  
agaccagaca tttcctttac tccaggggag atggccaaga gcgtctaaac ccctcattcc 1080  
tactcagcaa cctccagcct aacttgactg gggccaggag actggtggag atcatctttc 1140  
tgggctcaag gcctaggaca tcaggaccac tctgcaggac acaccgtcta tcgcgtcgat 1200



## 086,002 - SeqList.ST25.txt

actggcagat	gcggccccctg	ttccaacagc	tgctggtgaa	ccatgcagag	tgccaatatg	1260
tcagactcct	caggtcacat	tgcaaggtttc	gaacagcaaa	ccaacagggtg	acagatgcct	1320
tgaacaccag	cccaccgcac	ctcatggatt	tgctccgcct	gcacagcagt	ccctggcagg	1380
tatatggttt	tcttcgggcc	tgtctctgca	aggtggtgtc	tgctagtctc	tggggtagca	1440
ggcacaatga	gcgccgcttc	tttaagaact	taaagaagtt	catctcgttg	gggaaatacg	1500
gcaagctatc	actgcaggaa	ctgatgtgga	agatgaaagt	agaggattgc	cactggctcc	1560
gcagcagccc	ggggaaggac	cgtgtccccg	ctgcagagca	ccgtctgagg	gagaggatcc	1620
tggctacgtt	cctgttcttg	ctgatggaca	catacgtggg	acagctgctt	aggtcattct	1680
tttacatcac	agagagcaca	ttccagaaga	acaggctctt	cttctaccgt	aagagtgtgt	1740
ggagcaagct	gcagagcatt	ggagtcaggc	aacaccttga	gagagtgcgg	ctacgggagc	1800
tgtcacaaga	ggaggtcagg	catcaccagg	acacctggct	agccatgccc	atctgcagac	1860
tgcgcttcat	ccccaaagccc	aacggcctgc	ggccattgt	gaacatgagt	tatagcatgg	1920
gtaccagagc	tttgggcaga	aggaagcagg	cccagcattt	caccagcgt	ctcaagactc	1980
tcttcagcat	gctcaactat	gagcggacaa	aacatcctca	ccttatgggg	tcttctgtac	2040
tgggtatgaa	tgacatctac	aggacctggc	gggcctttgt	gctgcgtgtg	cgtgctctgg	2100
accagacacc	caggatgtac	tttgttaagg	cagatgtgac	cggggcctat	gatgccatcc	2160
cccagggtaa	gctgggtggag	gttgttgcca	atatgatcag	gcactcggag	agcacgtact	2220
gtatccgcca	gtatgcagtg	gtccggagag	atagccaagg	ccaagtccac	aagtccttta	2280
ggagacaggt	caccaccctc	tctgacctcc	agccatacat	gggccagttc	cttaagcatc	2340
tgcaaggattc	agatgccagt	gcactgagga	actccgttgt	catcgagcag	agcatctcta	2400
tgaatgagag	cagcagcagc	ctgtttgact	tcttcctgca	cttcctgcgt	cacagtgtcg	2460
taaagattgg	tgacaggtgc	tatacgcagt	gccagggcat	ccccagggc	tccagcctat	2520
ccaccctgct	ctgcagtctg	tgtttcggag	acatggagaa	caagctgttt	gctgaggtgc	2580
agcgggatgg	gttgctttta	cgttttgttg	atgactttct	gttggtgacg	cctcacttgg	2640
accaagcaaa	aaccttcctc	agcaccctgg	tccatggcgt	tcctgagtat	gggtgcatga	2700
taaacttgca	gaagacagtg	gtgaacttcc	ctgtggagcc	tggtaccctg	ggtggtgcag	2760
ctccatacca	gctgcctgct	cactgcctgt	ttccctgggtg	tggcttgctg	ctggacactc	2820
agactttgga	ggtgttctgt	gactactcag	gttatgccca	gacctcaatt	aagacgagcc	2880
tcaccttcca	gagtgtcttc	aaagctggga	agaccatgcg	gaacaagctc	ctgtcggctc	2940
tgcggttgaa	gtgtcacggt	ctatttctag	acttgcaagg	gaacagcctc	cagacagtct	3000
gcatcaatat	atacaagatc	ttcctgcttc	aggcctacag	gttccatgca	tgtgtgattc	3060

## 086,002 - SeqList.ST25.txt

```

agcttccctt tgaccagcgt gttaggaaga acctcacatt ctttctgggc atcatctcca 3120
gccaaagcatc ctgctgctat gctatcctga aggtcaagaa tccaggaatg acactaaagg 3180
cctctggctc ctttctcct gaagccgcac attggctctg ctaccaggcc ttctgctca 3240
agctggctgc tcattctgtc atctacaaat gtctcctggg acctctgagg acagcccaaa 3300
aactgctgtg ccggaagctc ccagaggcga caatgaccat ccttaaagct gcagctgacc 3360
cagccctaag cacagacttt cagaccattt tggactaacc ctgtctcctt ccgctagatg 3420
aacatg 3426

```

```

<210> 4
<211> 1122
<212> PRT
<213> Mus musculus

```

```
<400> 4
```

```
Met Thr Arg Ala Pro Arg Cys Pro Ala Val Arg Ser Leu Leu Arg Ser
1          5          10          15
```

```
Arg Tyr Arg Glu Val Trp Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20          25          30
```

```
Pro Glu Gly Arg Arg Leu Val Gln Pro Gly Asp Pro Lys Ile Tyr Arg
35          40          45
```

```
Thr Leu Val Ala Gln Cys Leu Val Cys Met His Trp Gly Ser Gln Pro
50          55          60
```

```
Pro Pro Ala Asp Leu Ser Phe His Gln Val Ser Ser Leu Lys Glu Leu
65          70          75          80
```

```
Val Ala Arg Val Val Gln Arg Leu Cys Glu Arg Asn Glu Arg Asn Val
85          90          95
```

```
Leu Ala Phe Gly Phe Glu Leu Leu Asn Glu Ala Arg Gly Gly Pro Pro
100          105          110
```

```
Met Ala Phe Thr Ser Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Ile
115          120          125
```

```
Glu Thr Leu Arg Val Ser Gly Ala Trp Met Leu Leu Leu Ser Arg Val
130          135          140
```

```
Gly Asp Asp Leu Leu Val Tyr Leu Leu Ala His Cys Ala Leu Tyr Leu
145          150          155          160
```

```
Leu Val Pro Pro Ser Cys Ala Tyr Gln Val Cys Gly Ser Pro Leu Tyr
Page 10
```

165

170

175

Gln Ile Cys Ala Thr Thr Asp Ile Trp Pro Ser Val Ser Ala Ser Tyr  
 180 185 190  
 Arg Pro Thr Arg Pro Val Gly Arg Asn Phe Thr Asn Leu Arg Phe Leu  
 195 200 205  
 Gln Gln Ile Lys Ser Ser Ser Arg Gln Glu Ala Pro Lys Pro Leu Ala  
 210 215 220  
 Leu Pro Ser Arg Gly Thr Lys Arg His Leu Ser Leu Thr Ser Thr Ser  
 225 230 235 240  
 Val Pro Ser Ala Lys Lys Ala Arg Cys Tyr Pro Val Pro Arg Val Glu  
 245 250 255  
 Glu Gly Pro His Arg Gln Val Leu Pro Thr Pro Ser Gly Lys Ser Trp  
 260 265 270  
 Val Pro Ser Pro Ala Arg Ser Pro Glu Val Pro Thr Ala Glu Lys Asp  
 275 280 285  
 Leu Ser Ser Lys Gly Lys Val Ser Asp Leu Ser Leu Ser Gly Ser Val  
 290 295 300  
 Cys Cys Lys His Lys Pro Ser Ser Thr Ser Leu Leu Ser Pro Pro Arg  
 305 310 315 320  
 Gln Asn Ala Phe Gln Leu Arg Pro Phe Ile Glu Thr Arg His Phe Leu  
 325 330 335  
 Tyr Ser Arg Gly Asp Gly Gln Glu Arg Leu Asn Pro Ser Phe Leu Leu  
 340 345 350  
 Ser Asn Leu Gln Pro Asn Leu Thr Gly Ala Arg Arg Leu Val Glu Ile  
 355 360 365  
 Ile Phe Leu Gly Ser Arg Pro Arg Thr Ser Gly Pro Leu Cys Arg Thr  
 370 375 380  
 His Arg Leu Ser Arg Arg Tyr Trp Gln Met Arg Pro Leu Phe Gln Gln  
 385 390 395 400  
 Leu Leu Val Asn His Ala Glu Cys Gln Tyr Val Arg Leu Leu Arg Ser  
 405 410 415

086,002 - SeqList.ST25.txt

His Cys Arg Phe Arg Thr Ala Asn Gln Gln Val Thr Asp Ala Leu Asn  
420 425 430

Thr Ser Pro Pro His Leu Met Asp Leu Leu Arg Leu His Ser Ser Pro  
435 440 445

Trp Gln Val Tyr Gly Phe Leu Arg Ala Cys Leu Cys Lys Val Val Ser  
450 455 460

Ala Ser Leu Trp Gly Thr Arg His Asn Glu Arg Arg Phe Phe Lys Asn  
465 470 475 480

Leu Lys Lys Phe Ile Ser Leu Gly Lys Tyr Gly Lys Leu Ser Leu Gln  
485 490 495

Glu Leu Met Trp Lys Met Lys Val Glu Asp Cys His Trp Leu Arg Ser  
500 505 510

Ser Pro Gly Lys Asp Arg Val Pro Ala Ala Glu His Arg Leu Arg Glu  
515 520 525

Arg Ile Leu Ala Thr Phe Leu Phe Trp Leu Met Asp Thr Tyr Val Val  
530 535 540

Gln Leu Leu Arg Ser Phe Phe Tyr Ile Thr Glu Ser Thr Phe Gln Lys  
545 550 555 560

Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser  
565 570 575

Ile Gly Val Arg Gln His Leu Glu Arg Val Arg Leu Arg Glu Leu Ser  
580 585 590

Gln Glu Glu Val Arg His His Gln Asp Thr Trp Leu Ala Met Pro Ile  
595 600 605

Cys Arg Leu Arg Phe Ile Pro Lys Pro Asn Gly Leu Arg Pro Ile Val  
610 615 620

Asn Met Ser Tyr Ser Met Gly Thr Arg Ala Leu Gly Arg Arg Lys Gln  
625 630 635 640

Ala Gln His Phe Thr Gln Arg Leu Lys Thr Leu Phe Ser Met Leu Asn  
645 650 655

Tyr Glu Arg Thr Lys His Pro His Leu Met Gly Ser Ser Val Leu Gly  
660 665 670

086,002 - SeqList.ST25.txt

Met Asn Asp Ile Tyr Arg Thr Trp Arg Ala Phe Val Leu Arg Val Arg  
675 680 685

Ala Leu Asp Gln Thr Pro Arg Met Tyr Phe Val Lys Ala Asp Val Thr  
690 695 700

Gly Ala Tyr Asp Ala Ile Pro Gln Gly Lys Leu Val Glu Val Val Ala  
705 710 715 720

Asn Met Ile Arg His Ser Glu Ser Thr Tyr Cys Ile Arg Gln Tyr Ala  
725 730 735

Val Val Arg Arg Asp Ser Gln Gly Gln Val His Lys Ser Phe Arg Arg  
740 745 750

Gln Val Thr Thr Leu Ser Asp Leu Gln Pro Tyr Met Gly Gln Phe Leu  
755 760 765

Lys His Leu Gln Asp Ser Asp Ala Ser Ala Leu Arg Asn Ser Val Val  
770 775 780

Ile Glu Gln Ser Ile Ser Met Asn Glu Ser Ser Ser Ser Leu Phe Asp  
785 790 795 800

Phe Phe Leu His Phe Leu Arg His Ser Val Val Lys Ile Gly Asp Arg  
805 810 815

Cys Tyr Thr Gln Cys Gln Gly Ile Pro Gln Gly Ser Ser Leu Ser Thr  
820 825 830

Leu Leu Cys Ser Leu Cys Phe Gly Asp Met Glu Asn Lys Leu Phe Ala  
835 840 845

Glu Val Gln Arg Asp Gly Leu Leu Leu Arg Phe Val Asp Asp Phe Leu  
850 855 860

Leu Val Thr Pro His Leu Asp Gln Ala Lys Thr Phe Leu Ser Thr Leu  
865 870 875 880

Val His Gly Val Pro Glu Tyr Gly Cys Met Ile Asn Leu Gln Lys Thr  
885 890 895

Val Val Asn Phe Pro Val Glu Pro Gly Thr Leu Gly Gly Ala Ala Pro  
900 905 910

Tyr Gln Leu Pro Ala His Cys Leu Phe Pro Trp Cys Gly Leu Leu Leu  
915 920 925

086,002 - SeqList.ST25.txt

Asp Thr Gln Thr Leu Glu Val Phe Cys Asp Tyr Ser Gly Tyr Ala Gln  
 930 935 940

Thr Ser Ile Lys Thr Ser Leu Thr Phe Gln Ser Val Phe Lys Ala Gly  
 945 950 955 960

Lys Thr Met Arg Asn Lys Leu Leu Ser Val Leu Arg Leu Lys Cys His  
 965 970 975

Gly Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Ile  
 980 985 990

Asn Ile Tyr Lys Ile Phe Leu Leu Gln Ala Tyr Arg Phe His Ala Cys  
 995 1000 1005

Val Ile Gln Leu Pro Phe Asp Gln Arg Val Arg Lys Asn Leu Thr  
 1010 1015 1020

Phe Phe Leu Gly Ile Ile Ser Ser Gln Ala Ser Cys Cys Tyr Ala  
 1025 1030 1035

Ile Leu Lys Val Lys Asn Pro Gly Met Thr Leu Lys Ala Ser Gly  
 1040 1045 1050

Ser Phe Pro Pro Glu Ala Ala His Trp Leu Cys Tyr Gln Ala Phe  
 1055 1060 1065

Leu Leu Lys Leu Ala Ala His Ser Val Ile Tyr Lys Cys Leu Leu  
 1070 1075 1080

Gly Pro Leu Arg Thr Ala Gln Lys Leu Leu Cys Arg Lys Leu Pro  
 1085 1090 1095

Glu Ala Thr Met Thr Ile Leu Lys Ala Ala Ala Asp Pro Ala Leu  
 1100 1105 1110

Ser Thr Asp Phe Gln Thr Ile Leu Asp  
 1115 1120

<210> 5  
 <211> 4170  
 <212> DNA  
 <213> Mesocricetus auratus

<400> 5  
 gggaggcccg gccggatctt gagcgcgatg cccgcgcgc cccgttgccg ggccgtgcgc 60  
 gctctgctgc gcagtcaata ccgtcaggtg tggccgctgg caaccttcgt gcggcgccctg 120

086,002 - SeqList.ST25.txt

ggacctgagg	gcaggcagct	tgtacaaccc	ggggacccaa	aggtcttccg	cacgttggtg	180
gcccgggtgcc	tagtgtgtgt	gccctgggac	tcacaacctc	cacctgctga	cctttccttc	240
caccagggtgt	catcactgaa	ggagctgggtg	gccagggctg	tgagagact	ctgcgagcgc	300
ggcgagagga	acgtgctgac	ttttggcttc	gcgctgctta	acggagccca	aggcggctct	360
cccatgacat	tcacaaccag	cgtgcgcagc	tacctgcca	actcggtgac	tgagtctctg	420
cgcgtcagtg	gtgcttggat	gcttctgctg	aaccgagtgg	gcgacgactt	gctgggtctac	480
ctgctggccc	gctgtgcgct	ttacctgctg	gtgccccga	gctgtgccta	ccagggtgtgc	540
ggctcacccc	tgtaccaa	ctgtgccacc	gcagaaacct	ggccttctgt	gtccccgcatc	600
tacaggccca	cacgacctgt	gggcagaaat	tttactcatc	ttggatccac	acaccgggtc	660
aggaacagca	gtcaccagga	agcatggaaa	ccccgcct	tgccatctcg	agaggcgaag	720
cggagtctaa	gcatcaccaa	tagaagtgtg	cctccatcta	agaaggccag	gtgcgatctg	780
gccccgagac	tggagaaggg	accctacagg	caggcagttc	caaccccatc	agacaaaaca	840
tgggtgccaa	atcctgccaa	gtcccatgca	gtgcctatta	gtagaactac	caaggaagat	900
ttgtcttccg	gggtgaaggc	acctggcctg	agtcgctctg	ggtcagtggtg	ctataaacac	960
aagcccagtt	ccacatccct	gcagtcacca	ctgtgccaaa	atgcctttca	gctcagacca	1020
tatactgaga	ccaaacgctt	cctctactct	agggaaaggtg	gccgagagag	gctgaacccc	1080
tcgttcctac	tcaacaacct	gcagcccagc	ttgactgggg	ccaggagact	ggtagagata	1140
ctctttctag	gcatgagacc	taggacatcg	ggaccactct	gtgggagacg	ccgcctatcg	1200
aagcgctact	ggcagatgcg	gcccctattc	cagcagttgc	ttgtgaacca	tgcgcggtgc	1260
ccgtatgtcc	ggctcctcag	gtcccattgc	aggtttcgga	ccgcagccca	ccagggtggca	1320
ggtgccttga	acaccaccag	cccacagcgc	ctcatgaatt	tgctccgtct	acacagcagt	1380
ccctggcagg	tatatggctt	tcttcaggcc	tgtgtcggaa	agctggtgcc	tccgggtctc	1440
tggggttccc	ggcacaacca	gcgacgcttc	tttaagaacg	tgaagcgggt	catctccttg	1500
gggaagtatg	acaagctgtc	gctgcaggag	ctgacgtgga	agatgaaagt	tcaagactgc	1560
aggtggcttc	gcagcagccc	agggaaacaac	tgtgtcccgg	ctgcagagca	ccgcacgagg	1620
gaaaggatcc	tggctgtgtt	cttgttctgg	ctgatggacg	cgtacgtggt	agagctgctt	1680
cggtcattct	tttacgtcac	agagaccact	ttccagaaga	accggctctt	cttctaccga	1740
aagagcatgt	ggagaaggct	gcagagcatt	ggagtcaggc	atcaccttga	gagagtgcgg	1800
ctacaagaac	tgtctcaaga	agaagtcagg	cagcgccagg	aggcctggcc	agccatgccc	1860
atctgcagac	tcggtttcat	ccccaaagccc	agtggctctc	ggcccatgtg	gaacatgagt	1920
tatatgggca	ccagagcctt	tgacaaaggg	aagcaggctc	agcatttcac	ccagtgtctc	1980

## 086,002 - SeqList.ST25.txt

aagactctgt	tcagcgtgct	caactatgaa	ctgacaaaac	atactaacct	tctgggggca	2040
tctgtactgg	gcctgaatga	tatctacagg	acctggcgga	ccttcgtact	gcgtgtgcgc	2100
actctggacc	cagcaccag	gatgtacttt	gttaaggcag	atgtgacagg	ggcatatgat	2160
gccatcccc	aggacaagct	tgtggagggt	attgccaaata	tgatcagaca	cccagacaac	2220
tcgtactgta	tccaccaata	tgcagtggtc	caaagagata	gacaaggcca	aatccacaag	2280
tccttcagga	gacagggtctc	caccctctct	gacctccagc	cacacatggg	ccagttcttg	2340
aagcatcttc	aggactcaga	caccagtgcg	ctgaggaact	ccgttgatcat	tgagcagagc	2400
ttatctctga	acgaggccag	cagcagcctg	ttcgacttct	tcctgcgctt	tgtgcgtaac	2460
agtgtcgtga	agatcgggtg	cagggtgctat	gtccagtgcc	agggcatccc	ccagggtccc	2520
agcctgtcca	ccctgctctg	cagtctgtgt	ttcggggaca	tggagaacaa	gctgtttgct	2580
gaagtgcagc	aggatgggct	gcttttgctg	tttgttgatg	actttctgtt	ggtgacacct	2640
cacctgggtcc	aggcggaagc	cttcctcagg	gccctcgtcc	gtggcatccc	tgagtacggc	2700
tgcatgataa	acttgacagaa	gacagtggta	aacttcctg	tggacgctgg	taccctggat	2760
ggcacagctc	cacaccagct	gcctgctcac	tgcctgtttc	cctgggtgtg	cttactgctg	2820
gacactcaga	ctctggagggt	gctctgtgac	tacactgggt	atgcccggac	ctcaattaag	2880
gccagcctca	ccttcacagc	caccttcaag	gcggggagga	acatgcgaca	gaagctctta	2940
gctgttttgc	ggttgaagtg	tcacagtctg	tttctagact	tgcagatgaa	tagccttcag	3000
acagtctgta	tcaatgtgta	caagatcttc	ctgcttcagg	cctacagggt	ccatgcgtgt	3060
gcgcttcagc	ttccctttga	ccaacatgtt	agaaagaacc	ccgcattctt	tctgagcatc	3120
atctccaaca	tagcatcctg	ctgctactcc	atcctgaagg	tcaagaatgc	aggaatgaca	3180
ctaaaggcca	aggggtgcctc	tggctcattt	cctcctgaag	ctgcacgttg	gctctgctac	3240
caagccttcc	tgctcaagct	ggctgggtcat	tctgtcacct	acaagtgtct	cctgggacct	3300
ctcaggacag	cacaaaaaca	gctgtgccc	aagctcccaa	gggcaacaat	ggccatcctt	3360
gagactgccg	ctgaccacagc	cctaagcaca	gactttcaga	ccattttgga	ctaaccctc	3420
cccttcagct	ggatgaacat	gggcattgta	gcctcaccac	tcctggatgc	atgccacaag	3480
agggactgac	ctgttgtgag	gccagtttgc	cctccaaaac	atgtgccagg	gctgtagtat	3540
gggggttgtc	cctgtgccgt	gtttcctgtg	gtggacttga	tttctttcct	gatgcctccg	3600
gggaagcagc	tcccaccctc	ctcgggtggca	gggatccact	agccagtaac	accagacaga	3660
ggagaagatg	cctgggcact	gggacagtgt	gcacggatct	gagatgccc	gccctgtgtc	3720
tcttcacatc	taaccatgg	agcctttccc	aacgggggtca	cagtagaaag	tgtttttggg	3780
gggcttacag	ttttaaggt	ttagaatcta	tgatcatcac	ggtagggagc	atggcagcaa	3840
ggaggcaggc	atgtgtcttc	tcacgcctaa	ccgaggagcc	ttttccaatg	ggccagtggg	3900



086,002 - SeqList.ST25.txt

gtcagaatgt ctcagagatg aaaacaggac tttgaactga tgtggggggtt tgaagatgtg 3960  
tagtccccac agaccctgtg gttcaaatgc ttggcctatt ggaatgtcac tattaggagg 4020  
tgtggcttgt tggaggaagt gtgtctgtca ctgtgaggac agggctttca ggtctcatat 4080  
atgctcaaac tgtgccaat acacagacga cttctgctgc tatgaataaa gatgtagaac 4140  
tctaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4170

<210> 6  
<211> 1128  
<212> PRT  
<213> Mesocricetus auratus

<400> 6

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ala Leu Leu Arg Ser  
1 5 10 15

Gln Tyr Arg Gln Val Trp Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30

Pro Glu Gly Arg Gln Leu Val Gln Pro Gly Asp Pro Lys Val Phe Arg  
35 40 45

Thr Leu Val Ala Arg Cys Leu Val Cys Val Pro Trp Asp Ser Gln Pro  
50 55 60

Pro Pro Ala Asp Leu Ser Phe His Gln Val Ser Ser Leu Lys Glu Leu  
65 70 75 80

Val Ala Arg Val Val Gln Arg Leu Cys Glu Arg Gly Glu Arg Asn Val  
85 90 95

Leu Thr Phe Gly Phe Ala Leu Leu Asn Gly Ala Gln Gly Gly Pro Pro  
100 105 110

Met Thr Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Ser Val Thr  
115 120 125

Glu Ser Leu Arg Val Ser Gly Ala Trp Met Leu Leu Leu Asn Arg Val  
130 135 140

Gly Asp Asp Leu Leu Val Tyr Leu Leu Ala Arg Cys Ala Leu Tyr Leu  
145 150 155 160

Leu Val Pro Pro Ser Cys Ala Tyr Gln Val Cys Gly Ser Pro Leu Tyr  
165 170 175

## 086,002 - SeqList.ST25.txt

Gln Ile Cys Ala Thr Ala Glu Thr Trp Pro Ser Val Ser Arg Ile Tyr  
 180 185 190  
 Arg Pro Thr Arg Pro Val Gly Arg Asn Phe Thr His Leu Gly Ser Thr  
 195 200 205  
 His Arg Val Arg Asn Ser Ser His Gln Glu Ala Trp Lys Pro Pro Pro  
 210 215 220  
 Leu Pro Ser Arg Glu Ala Lys Arg Ser Leu Ser Ile Thr Asn Arg Ser  
 225 230 235 240  
 Val Pro Pro Ser Lys Lys Ala Arg Cys Asp Leu Ala Pro Arg Leu Glu  
 245 250 255  
 Lys Gly Pro Tyr Arg Gln Ala Val Pro Thr Pro Ser Asp Lys Thr Trp  
 260 265 270  
 Val Pro Asn Pro Ala Lys Ser His Ala Val Pro Ile Ser Arg Thr Thr  
 275 280 285  
 Lys Glu Asp Leu Ser Ser Gly Val Lys Ala Pro Gly Leu Ser Arg Ser  
 290 295 300  
 Gly Ser Val Cys Tyr Lys His Lys Pro Ser Ser Thr Ser Leu Gln Ser  
 305 310 315 320  
 Pro Leu Cys Gln Asn Ala Phe Gln Leu Arg Pro Tyr Thr Glu Thr Lys  
 325 330 335  
 Arg Phe Leu Tyr Ser Arg Glu Gly Gly Arg Glu Arg Leu Asn Pro Ser  
 340 345 350  
 Phe Leu Leu Asn Asn Leu Gln Pro Ser Leu Thr Gly Ala Arg Arg Leu  
 355 360 365  
 Val Glu Ile Leu Phe Leu Gly Met Arg Pro Arg Thr Ser Gly Pro Leu  
 370 375 380  
 Cys Gly Arg Arg Arg Leu Ser Lys Arg Tyr Trp Gln Met Arg Pro Leu  
 385 390 395 400  
 Phe Gln Gln Leu Leu Val Asn His Ala Arg Cys Pro Tyr Val Arg Leu  
 405 410 415  
 Leu Arg Ser His Cys Arg Phe Arg Thr Ala Ala His Gln Val Ala Gly  
 420 425 430

086,002 - SeqList.ST25.txt

Ala Leu Asn Thr Thr Ser Pro Gln Arg Leu Met Asn Leu Leu Arg Leu  
435 440 445

His Ser Ser Pro Trp Gln Val Tyr Gly Phe Leu Gln Ala Cys Val Gly  
450 455 460

Lys Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Gln Arg Arg  
465 470 475 480

Phe Phe Lys Asn Val Lys Arg Phe Ile Ser Leu Gly Lys Tyr Asp Lys  
485 490 495

Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Lys Val Gln Asp Cys Arg  
500 505 510

Trp Leu Arg Ser Ser Pro Gly Asn Asn Cys Val Pro Ala Ala Glu His  
515 520 525

Arg Thr Arg Glu Arg Ile Leu Ala Val Phe Leu Phe Trp Leu Met Asp  
530 535 540

Ala Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr  
545 550 555 560

Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Met Trp Arg  
565 570 575

Arg Leu Gln Ser Ile Gly Val Arg His His Leu Glu Arg Val Arg Leu  
580 585 590

Gln Glu Leu Ser Gln Glu Glu Val Arg Gln Arg Gln Glu Ala Trp Pro  
595 600 605

Ala Met Pro Ile Cys Arg Leu Arg Phe Ile Pro Lys Pro Ser Gly Leu  
610 615 620

Arg Pro Ile Val Asn Met Ser Tyr Met Gly Thr Arg Ala Phe Asp Lys  
625 630 635 640

Gly Lys Gln Ala Gln His Phe Thr Gln Cys Leu Lys Thr Leu Phe Ser  
645 650 655

Val Leu Asn Tyr Glu Leu Thr Lys His Thr Asn Leu Leu Gly Ala Ser  
660 665 670

Val Leu Gly Leu Asn Asp Ile Tyr Arg Thr Trp Arg Thr Phe Val Leu  
675 680 685

086,002 - SeqList.ST25.txt

Arg Val Arg Thr Leu Asp Pro Ala Pro Arg Met Tyr Phe Val Lys Ala  
690 695 700

Asp Val Thr Gly Ala Tyr Asp Ala Ile Pro Gln Asp Lys Leu Val Glu  
705 710 715 720

Val Ile Ala Asn Met Ile Arg His Pro Asp Asn Ser Tyr Cys Ile His  
725 730 735

Gln Tyr Ala Val Val Gln Arg Asp Arg Gln Gly Gln Ile His Lys Ser  
740 745 750

Phe Arg Arg Gln Val Ser Thr Leu Ser Asp Leu Gln Pro His Met Gly  
755 760 765

Gln Phe Leu Lys His Leu Gln Asp Ser Asp Thr Ser Ala Leu Arg Asn  
770 775 780

Ser Val Val Ile Glu Gln Ser Leu Ser Leu Asn Glu Ala Ser Ser Ser  
785 790 795 800

Leu Phe Asp Phe Phe Leu Arg Phe Val Arg Asn Ser Val Val Lys Ile  
805 810 815

Gly Gly Arg Cys Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ser  
820 825 830

Leu Ser Thr Leu Leu Cys Ser Leu Cys Phe Gly Asp Met Glu Asn Lys  
835 840 845

Leu Phe Ala Glu Val Gln Gln Asp Gly Leu Leu Leu Arg Phe Val Asp  
850 855 860

Asp Phe Leu Leu Val Thr Pro His Leu Val Gln Ala Glu Ala Phe Leu  
865 870 875 880

Arg Ala Leu Val Arg Gly Ile Pro Glu Tyr Gly Cys Met Ile Asn Leu  
885 890 895

Gln Lys Thr Val Val Asn Phe Pro Val Asp Ala Gly Thr Leu Asp Gly  
900 905 910

Thr Ala Pro His Gln Leu Pro Ala His Cys Leu Phe Pro Trp Cys Gly  
915 920 925

Leu Leu Leu Asp Thr Gln Thr Leu Glu Val Leu Cys Asp Tyr Thr Gly

930

935

940

Tyr Ala Arg Thr Ser Ile Lys Ala Ser Leu Thr Phe Gln Arg Thr Phe  
 945 950 955 960

Lys Ala Gly Arg Asn Met Arg Gln Lys Leu Leu Ala Val Leu Arg Leu  
 965 970 975

Lys Cys His Ser Leu Phe Leu Asp Leu Gln Met Asn Ser Leu Gln Thr  
 980 985 990

Val Cys Ile Asn Val Tyr Lys Ile Phe Leu Leu Gln Ala Tyr Arg Phe  
 995 1000 1005

His Ala Cys Ala Leu Gln Leu Pro Phe Asp Gln His Val Arg Lys  
 1010 1015 1020

Asn Pro Ala Phe Phe Leu Ser Ile Ile Ser Asn Ile Ala Ser Cys  
 1025 1030 1035

Cys Tyr Ser Ile Leu Lys Val Lys Asn Ala Gly Met Thr Leu Lys  
 1040 1045 1050

Ala Lys Gly Ala Ser Gly Ser Phe Pro Pro Glu Ala Ala Arg Trp  
 1055 1060 1065

Leu Cys Tyr Gln Ala Phe Leu Leu Lys Leu Ala Gly His Ser Val  
 1070 1075 1080

Thr Tyr Lys Cys Leu Leu Gly Pro Leu Arg Thr Ala Gln Lys Gln  
 1085 1090 1095

Leu Cys Arg Lys Leu Pro Arg Ala Thr Met Ala Ile Leu Glu Thr  
 1100 1105 1110

Ala Ala Asp Pro Ala Leu Ser Thr Asp Phe Gln Thr Ile Leu Asp  
 1115 1120 1125

&lt;210&gt; 7

&lt;211&gt; 1758

&lt;212&gt; DNA

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 7

aggtcattct ttacatcac agagagcaca ttccagaaga acaggctctt cttctaccgt 60

aagagtgtgt ggagcaagct gcagagcatt ggagtcaggc aacaccttga gagagtgcgg 120

ctacggggagc tgtcacaaga ggaggtcagg catcaccagg acacctggct agccatgccc 180

## 086,002 - SeqList.ST25.txt

atctgcagac	tgcgcttcat	ccccaaagccc	aacggcctgc	ggcccattgt	gaacatgagt	240
tatagcatgg	gtaccagagc	tttgggcaga	aggaagcagg	cccagcattt	cacccagcgt	300
ctcaagactc	tcttcagcat	gctcaactat	gagcggacaa	aacatcctca	ccttatgggg	360
tcttctgtac	tgggtatgaa	tgacatctac	aggacctggc	gggcctttgt	gctgcgtgtg	420
cgtgctctgg	accagacacc	caggatgtac	tttgtaagg	cagatgtgac	cggggcctat	480
gatgccatcc	cccagggtaa	gctgggtggag	gttggttgcca	atatgatcag	gcactcggag	540
agcacgtact	gtatccgcca	gtatgcagtg	gtccggagag	atagccaagg	ccaagtccac	600
aagtccttta	ggagacaggt	caccaccctc	tctgacctcc	agccatacat	gggccagttc	660
cttaagcatc	tgaggatttc	agatgccagt	gcactgagga	actccgttgt	catcgagcag	720
agcatctcta	tgaatgagag	cagcagcagc	ctgtttgact	tcttcctgca	cttcctgcgt	780
cacagtgtcg	taaagattgg	tgacaggtgc	tatacgcagt	gccagggcat	ccccagggc	840
tccagcctat	ccaccctgct	ctgcagtctg	tgtttcggag	acatggagaa	caagctgttt	900
gctgaggtgc	agcgggatgg	gttgctttta	cgttttgttg	atgactttct	gttggtgacg	960
cctcacttgg	accaagcaaa	aaccttcctc	agcaccctgg	tccatggcgt	tcctgagtat	1020
gggtgcatga	taaacttgca	gaagacagtg	gtgaacttcc	ctgtggagcc	tggtaccctg	1080
ggtggtgcag	ctccatacca	gctgcctgct	cactgcctgt	ttccctggtg	tggcttgctg	1140
ctggacactc	agactttgga	ggtgttctgt	gactactcag	gttatgcca	gacctcaatt	1200
aagacgagcc	tcaccttcca	gagtgtcttc	aaagctggga	agaccatgcg	gaacaagctc	1260
ctgtcgggtct	tgcggttgaa	gtgtcacggt	ctatttctag	acttgcaggt	gaacagcctc	1320
cagacagtct	gcatcaatat	atacaagatc	ttcctgcttc	aggcctacag	gttccatgca	1380
tgtgtgattc	agcttccctt	tgaccagcgt	gttaggaaga	acctcacatt	ctttctgggc	1440
atcatctcca	gccaagcatc	ctgctgctat	gctatcctga	aggtcaagaa	tccaggaatg	1500
acactaaagg	cctctggctc	ctttcctcct	gaagccgcac	attggctctg	ctaccaggcc	1560
ttcctgctca	agctggctgc	tcattctgtc	atctacaaat	gtctcctggg	acctctgagg	1620
acagcccaaa	aactgctgtg	ccggaagctc	ccagaggcga	caatgaccat	ccttaaagct	1680
gcagctgacc	cagccctaag	cacagacttt	cagaccattt	tggactaacc	ctgtctcctt	1740
ccgctagatg	aacatggc					1758

&lt;210&gt; 8

&lt;211&gt; 575

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 8

Arg Ser Phe Phe Tyr Ile Thr Glu Ser Thr Phe Gln Lys Asn Arg Leu

```

1              5              10              15
Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Val
      20      25      30
Arg Gln His Leu Glu Arg Val Arg Leu Arg Glu Leu Ser Gln Glu Glu
      35      40      45
Val Arg His His Gln Asp Thr Trp Leu Ala Met Pro Ile Cys Arg Leu
      50      55      60
Arg Phe Ile Pro Lys Pro Asn Gly Leu Arg Pro Ile Val Asn Met Ser
      65      70      75      80
Tyr Ser Met Gly Thr Arg Ala Leu Gly Arg Arg Lys Gln Ala Gln His
      85      90      95
Phe Thr Gln Arg Leu Lys Thr Leu Phe Ser Met Leu Asn Tyr Glu Arg
      100      105      110
Thr Lys His Pro His Leu Met Gly Ser Ser Val Leu Gly Met Asn Asp
      115      120      125
Ile Tyr Arg Thr Trp Arg Ala Phe Val Leu Arg Val Arg Ala Leu Asp
      130      135      140
Gln Thr Pro Arg Met Tyr Phe Val Lys Ala Asp Val Thr Gly Ala Tyr
      145      150      155      160
Asp Ala Ile Pro Gln Gly Lys Leu Val Glu Val Val Ala Asn Met Ile
      165      170      175
Arg His Ser Glu Ser Thr Tyr Cys Ile Arg Gln Tyr Ala Val Val Arg
      180      185      190
Arg Asp Ser Gln Gly Gln Val His Lys Ser Phe Arg Arg Gln Val Thr
      195      200      205
Thr Leu Ser Asp Leu Gln Pro Tyr Met Gly Gln Phe Leu Lys His Leu
      210      215      220
Gln Asp Ser Asp Ala Ser Ala Leu Arg Asn Ser Val Val Ile Glu Gln
      225      230      235      240
Ser Ile Ser Met Asn Glu Ser Ser Ser Ser Leu Phe Asp Phe Phe Leu
      245      250      255

```

086,002 - SeqList.ST25.txt

His Phe Leu Arg His Ser Val Val Lys Ile Gly Asp Arg Cys Tyr Thr  
260 265 270

Gln Cys Gln Gly Ile Pro Gln Gly Ser Ser Leu Ser Thr Leu Leu Cys  
275 280 285

Ser Leu Cys Phe Gly Asp Met Glu Asn Lys Leu Phe Ala Glu Val Gln  
290 295 300

Arg Asp Gly Leu Leu Leu Arg Phe Val Asp Asp Phe Leu Leu Val Thr  
305 310 315 320

Pro His Leu Asp Gln Ala Lys Thr Phe Leu Ser Thr Leu Val His Gly  
325 330 335

Val Pro Glu Tyr Gly Cys Met Ile Asn Leu Gln Lys Thr Val Val Asn  
340 345 350

Phe Pro Val Glu Pro Gly Thr Leu Gly Gly Ala Ala Pro Tyr Gln Leu  
355 360 365

Pro Ala His Cys Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Gln  
370 375 380

Thr Leu Glu Val Phe Cys Asp Tyr Ser Gly Tyr Ala Gln Thr Ser Ile  
385 390 395 400

Lys Thr Ser Leu Thr Phe Gln Ser Val Phe Lys Ala Gly Lys Thr Met  
405 410 415

Arg Asn Lys Leu Leu Ser Val Leu Arg Leu Lys Cys His Gly Leu Phe  
420 425 430

Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Ile Asn Ile Tyr  
435 440 445

Lys Ile Phe Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Ile Gln  
450 455 460

Leu Pro Phe Asp Gln Arg Val Arg Lys Asn Leu Thr Phe Phe Leu Gly  
465 470 475 480

Ile Ile Ser Ser Gln Ala Ser Cys Cys Tyr Ala Ile Leu Lys Val Lys  
485 490 495

Asn Pro Gly Met Thr Leu Lys Ala Ser Gly Ser Phe Pro Pro Glu Ala  
500 505 510



086,002 - SeqList.ST25.txt

Ala His Trp Leu Cys Tyr Gln Ala Phe Leu Leu Lys Leu Ala Ala His  
515 520 525

Ser Val Ile Tyr Lys Cys Leu Leu Gly Pro Leu Arg Thr Ala Gln Lys  
530 535 540

Leu Leu Cys Arg Lys Leu Pro Glu Ala Thr Met Thr Ile Leu Lys Ala  
545 550 555 560

Ala Ala Asp Pro Ala Leu Ser Thr Asp Phe Gln Thr Ile Leu Asp  
565 570 575

<210> 9

<211> 2231

<212> DNA

<213> Canis familiaris

<400> 9

atgccgcgag cgccccggtg ccgcgccgtg cgcgccctgc tgcggggccg ctaccgggag	60
gtgctgcccc tggccacctt cctgcggcgc ctggggcccc cgggccggct gctcgtgcgg	120
cgcggggacc cggcggcctt ccgcgcgctg gtggcgcagt gcctggtgtg cgtgccctgg	180
ggcgcgcggc cgccccccgc cgccccgtgc ttccgccagc tggctttcgg cttcgccctg	240
ctggacggag cgcgcgggcg gccccccgtg gccttcacga ccagcgtgcg cagctacctg	300
cccaacacgg taaccgagac cctgcgcggc agcggcgcct gggggctgct gctgcgccgc	360
gtgggcgacg atgtgctcac ccacctgctg gcgcgctgcg cgctctacct gctggtggct	420
ccgagctgcg cctaccaggt gtgcggggccg ccgtctacga cctctgcgcc ccgcctctc	480
tgccgctccc ggccccgctc cccgctcccc gctccccgct cggccggccg ggctcgggac	540
ctcagaccca cacgccaggc cagaactcgg ccagcgcggg gcagcccgga gcggtcctct	600
ggaagcgcca gccagtggcg gagcagacgg cgccacaggc cttcccaggc cacagctcct	660
gtagcaagcc ggggtgtacac ctgccgggcg cttccccagc tggcctggga gggaggcccc	720
ccggactcgt ccaaccaccc cagcctggat acatctccgg ggccccaggg agtaccat	780
gaccagcac accccgagac caaacgcttc ctctactgct cgggtggcag ggagcggctg	840
cgccctcct tcctgctcag tgccctgccg cctaccctgg gggccgcaa actcgtggag	900
accatctttc tgggctctgc gccccagaag ccaggggccc cccgcaggat gcgccgcctg	960
cctgcccgtc actggcgaat gaggcccctg ttccaggagc tgcttgggaa ccacgcccgg	1020
tgccctacc gtgcgtcct caggaccac tgcccgttc gggccatggc cgctaaggag	1080
gggtctggca accaggcaca caggggagtg ggcattctgc ccctggagag gccagtagca	1140
gccccccagg agcagacgga ctccacacgc ctggtacagc tcctccgaca gcacagcagc	1200

086,002 - SeqList.ST25.txt

ccctggcagg tgtatgcctt cctgagggcc tgcctgtgct ggctggtgcc cactggactc 1260  
 tggggctcca ggcacaacca gcgccgttc ttgaggaacg tgaagaagtt catctccctg 1320  
 ggaaagcacg ctaagctctc cctgcaggaa ctgacgtgga agatgaaggt gcgggactgc 1380  
 acctggctgc acgggaaccc aggtgaggag tgcagagtga gcaggtgcct ggttggccta 1440  
 caggaaggac caggctcaca gcccagtggt ggtaggcccc tccctcccaa ccatccatct 1500  
 cggaacaccc cttcctctgt tgggccggca gcgactgccc tgcctgcctc tcagcccccc 1560  
 gactcccgtc acaaactagt ccccatcccc agaggctgcc gggctgtcca catctgctgc 1620  
 caggagtcac gagacatcac gaaatgagct cttggtggcg gccctcatcc cttacccccg 1680  
 ggacacacatg gctcctcata ggctgtgcgc cacaactctt caatagtgtg cacctccgag 1740  
 aactgtcaga agcagaggtc aggagacacc gggaagccag acctgctctg ctgacctcca 1800  
 gactccgctt cctccccaag cctagtgggc tgcggccgat tgtgaatatg gactacatca 1860  
 tgggagccag aacattccac agagacaaga aggtccagca tctcacctca caactgaaga 1920  
 cactgttcag tgtcctgaac tatgagcggg cccggcgccc cagcctccta ggggcctcca 1980  
 tgctgggcat ggacgacatc cacagggcct ggcgcacctt tgtgctacgc atacgggccc 2040  
 agaatccggc accccagctg tactttgtca aggtggacgt gacgggggca tatgacgccc 2100  
 tccctcagga caggctggta gaggtgattg ccaatgtgat caggcctcag gaaagcacat 2160  
 actgcgtgcg ccactatgcc gtggtccaga ggactgcccg gggacacgtc cgcaaggcct 2220  
 tcaaaagaca c 2231

<210> 10  
 <211> 743  
 <212> PRT  
 <213> Canis familiaris  
 <400> 10

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ala Leu Leu Arg Gly  
 1 5 10 15

Arg Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Leu Arg Arg Leu Gly  
 20 25 30

Pro Pro Gly Arg Leu Leu Val Arg Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Gly Ala Arg Pro  
 50 55 60

Pro Pro Ala Ala Pro Cys Phe Arg Gln Leu Ala Phe Gly Phe Ala Leu  
 65 70 75 80

086,002 - SeqList.ST25.txt

Leu Asp Gly Ala Arg Gly Gly Pro Pro Val Ala Phe Thr Thr Ser Val  
 85 90 95  
 Arg Ser Tyr Leu Pro Asn Thr Val Thr Glu Thr Leu Arg Gly Ser Gly  
 100 105 110  
 Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Thr His  
 115 120 125  
 Leu Leu Ala Arg Cys Ala Leu Tyr Leu Leu Val Ala Pro Ser Cys Ala  
 130 135 140  
 Tyr Gln Val Cys Gly Pro Pro Ser Thr Thr Ser Ala Pro Pro Pro Leu  
 145 150 155 160  
 Cys Arg Ser Arg Pro Arg Ser Pro Leu Pro Ala Pro Arg Ser Ala Gly  
 165 170 175  
 Arg Ala Arg Asp Leu Arg Pro Thr Arg Gln Ala Arg Thr Arg Pro Ala  
 180 185 190  
 Arg Gly Ser Pro Glu Arg Ser Ser Gly Ser Ala Ser Gln Trp Arg Ser  
 195 200 205  
 Arg Arg Arg His Arg Pro Ser Gln Ala Thr Ala Pro Val Ala Ser Arg  
 210 215 220  
 Val Tyr Thr Cys Arg Ala Leu Pro Gln Leu Ala Trp Glu Gly Gly Pro  
 225 230 235 240  
 Pro Asp Ser Ser Asn His Pro Ser Leu Asp Thr Ser Pro Gly Pro Gln  
 245 250 255  
 Gly Val Pro His Asp Pro Ala His Pro Glu Thr Lys Arg Phe Leu Tyr  
 260 265 270  
 Cys Ser Gly Gly Arg Glu Arg Leu Arg Pro Ser Phe Leu Leu Ser Ala  
 275 280 285  
 Leu Pro Pro Thr Leu Gly Ala Arg Lys Leu Val Glu Thr Ile Phe Leu  
 290 295 300  
 Gly Ser Ala Pro Gln Lys Pro Gly Ala Ala Arg Arg Met Arg Arg Leu  
 305 310 315 320  
 Pro Ala Arg Tyr Trp Arg Met Arg Pro Leu Phe Gln Glu Leu Leu Gly  
 325 330 335

086,002 - SeqList.ST25.txt

Asn His Ala Arg Cys Pro Tyr Arg Ala Leu Leu Arg Thr His Cys Pro  
 340 345 350  
 Leu Arg Ala Met Ala Ala Lys Glu Gly Ser Gly Asn Gln Ala His Arg  
 355 360 365  
 Gly Val Gly Ile Cys Pro Leu Glu Arg Pro Val Ala Ala Pro Gln Glu  
 370 375 380  
 Gln Thr Asp Ser Thr Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser  
 385 390 395 400  
 Pro Trp Gln Val Tyr Ala Phe Leu Arg Ala Cys Leu Cys Trp Leu Val  
 405 410 415  
 Pro Thr Gly Leu Trp Gly Ser Arg His Asn Gln Arg Arg Phe Leu Arg  
 420 425 430  
 Asn Val Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu  
 435 440 445  
 Gln Glu Leu Thr Trp Lys Met Lys Val Arg Asp Cys Thr Trp Leu His  
 450 455 460  
 Gly Asn Pro Gly Glu Glu Cys Arg Val Ser Arg Cys Leu Val Gly Leu  
 465 470 475 480  
 Gln Glu Gly Pro Gly Ser Gln Pro Glu Cys Gly Arg Pro Leu Pro Pro  
 485 490 495  
 Asn His Pro Ser Glu His Pro Phe Leu Cys Trp Ala Gly Ser Asp Cys  
 500 505 510  
 Pro Ala Cys Leu Ser Ala Pro Arg Leu Pro Ser Gln Thr Ser Pro His  
 515 520 525  
 Pro Gln Arg Leu Pro Gly Cys Pro His Leu Leu Pro Gly Val Met Arg  
 530 535 540  
 His His Glu Met Ser Ser Trp Trp Arg Pro Ser Ser Pro Tyr Pro Gly  
 545 550 555 560  
 His Thr Trp Leu Leu Ile Gly Cys Ala Pro Gln Leu Phe Asn Ser Val  
 565 570 575  
 His Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Arg His Arg Glu Ala  
 Page 28



580

Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Leu Pro Lys Pro Ser  
595 600 605

Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Ile Met Gly Ala Arg Thr  
610 615 620

Phe His Arg Asp Lys Lys Val Gln His Leu Thr Ser Gln Leu Lys Thr  
625 630 635 640

Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Ser Leu Leu  
645 650 655

Gly Ala Ser Met Leu Gly Met Asp Asp Ile His Arg Ala Trp Arg Thr  
660 665 670

Phe Val Leu Arg Ile Arg Ala Gln Asn Pro Ala Pro Gln Leu Tyr Phe  
675 680 685

Val Lys Val Asp Val Thr Gly Ala Tyr Asp Ala Leu Pro Gln Asp Arg  
690 695 700

Leu Val Glu Val Ile Ala Asn Val Ile Arg Pro Gln Glu Ser Thr Tyr  
705 710 715 720

Cys Val Arg His Tyr Ala Val Val Gln Arg Thr Ala Arg Gly His Val  
725 730 735

Arg Lys Ala Phe Lys Arg His  
740

<210> 11  
<211> 2855  
<212> DNA  
<213> Homo sapiens

<400> 11  
atgcccgcgc ccccgtagcg gccgtgagcc ctgctgagca gcctaccgga ggtggccgct 60  
ggcaccttcg tgcggcgctt ggggcccagg gcggcgctgt gcaccgggga cccgggcttc 120  
cgccgtggtg gccagtgcc tgtgtgagtg ccctgggcca cgcggggcgc cgcttccttc 180  
cccaggtgtc tctgaagagc tggtagccgg ttgcagagct ctgcgagcgc cggaaacgtg 240  
ctggcttttg cttcgagctg ctacggggcc gggcgggccc ctggccttca caccagcgtg 300  
cgcagctacc tgccaacac ggtacgagcc tgcggcagg gctgggctct gctggccggt 360  
gggcgacgac tgctggtcac ctgctggccg ctggcgctta ctgctggtgc ccagctggcc 420

## 086,002 - SeqList.ST25.txt

taccaggtgt	gcgggcccct	gtaccatctg	gccccactg	gccctcgcca	gccccgcct	480
gggataacgc	gacgagtcca	ggagcagaac	cccggcctgc	cactcgggcg	aggggcggcc	540
atgaagtgtg	cccaagagcc	aggcgcccgg	cggagggccc	acaggcaggc	ccccgcaacg	600
gtccaagtcg	tccgggtgcc	tccgaaagtc	ttggaggctg	ccgagtcctc	tcgtggcaac	660
acagccgtcc	acatcgcgtc	accaccccaa	gctcacccat	acgagaccaa	accttcctct	720
actccgaggt	ggcgagcggc	tgccccctct	cctactcagc	cctgcgccac	tgactggggc	780
cggagactgt	ggagacatct	ttctgggctc	aggccggaca	ggccccgagg	acccgcctcc	840
gctactggca	atgcggcccc	tgttccagag	ctgcttgga	ccagccgtgc	cctaggctcc	900
tcaggccatg	cgttcgcgcg	ccacaggtgc	ggcctgacac	ccccccgcct	tgatgctccg	960
cgcacagcag	ccctggcagg	ttatggcttc	tcgggcctgc	tgcgctggtg	cccggctctg	1020
gggtccaggc	acaacagcgc	cgcttcttag	aactaagaag	ttcatctcct	ggggaagagc	1080
aagcttcctg	caggactgac	gtggaagatg	aagtcggact	gctggctcgc	agagcccagg	1140
gagactgtgt	ccggctgcag	agcaccgcga	ggagaggatc	ctggctgttc	ctgctggctg	1200
atgacctacg	tggtagctgc	taggtcattc	ttttacgtca	cagagaccac	attccagaag	1260
aacaggctct	tcttctaccg	aagagtgtgt	ggagcaagct	gcagagcatt	ggagtcaggc	1320
aacaccttga	gagagtgcgg	ctacgggagc	tgtcacaaga	agaggtcagg	cacaccagga	1380
gcctggccag	ccatgcccac	ctgcagactg	cgcttcatcc	ccaagcccaa	cggctgcggc	1440
ccattgtgaa	catgagttat	acatgggacc	agagcttggc	agaggggaagc	aggcccagca	1500
tttcacccag	cgtctcaaga	ctctgttcag	cgtgctcaac	tatgagcgga	caaaacatcc	1560
taccttctgg	gggctctgta	ctgggcatga	atgacatcta	caggacctgg	cggacctttg	1620
tgctgcgtgt	gcggtctctg	acccgcaccc	aggatgtact	ttgttaaggc	agatgtgacg	1680
gggctatgat	gccatcccc	aggacaagct	ggtggagggt	attgccaata	tgatcaggca	1740
ccggagagca	cgtactgtat	ccgccagtat	gcagtgggtc	agagagatag	ccaaggccaa	1800
gtccacaagt	ccttcaggag	acaggtccca	ccctctctga	cctccagcca	tacatgggcc	1860
agttctaagc	atctgcagga	tcagaccagt	gcctgaggaa	ctccgttgtc	atcgagcaga	1920
gctctcttga	atgagcagca	gcagcctggt	gacttcttcc	tgcttctgct	gtcacagtgt	1980
cgtaagatgg	tgaggtgct	atcagtgcc	gggcatcccc	cagggtcca	gccttccacc	2040
ctgctctgca	gtctgtgttt	cgggacatgg	agaacaagct	gtttgctgag	gtgcagcggg	2100
atgggtgctt	ttcgttttgt	tgatgacttt	ctgttggtga	ccctcactgg	ccagcaaaac	2160
cttcctcaga	ccctggtcct	ggcgctctga	gtatggtgca	tgataaaactt	gcagaagaca	2220
gtggtgaact	tccctgtgga	ctggtaccct	gggtggcagc	tccaaccagc	tgctgtctca	2280
ctgcctgttt	ccctggtgtg	gcttgctgct	ggacactcag	acttggagggt	gtctgtgact	2340

086,002 - SeqList.ST25.txt

```

actcggttat gcccgacctc aattaagcag cctcaccttc cagggcttca agctgggaga 2400
catgcgacaa gctctcggtc ttgcggttga agtgtcacgt cttttctaga cttgcaggtg 2460
aacagcctcc agacagtctg catcaatatt acaagatctt cctgcttcag gcctacaggt 2520
tccatgcatg tgtgttcagc ttccctttga ccagctgtta ggaagaaccc acattctttc 2580
tggcatcatc tccacagcat cctgctgcta catcctgaag gtcaagaatc aggaatgaca 2640
ctaaaggcct ctggctcttt cctcctgaag ccgcacattg gctctgctac cagccttcct 2700
gctcaagctg gctgtcattc tgtcactaca atgtctcctg ggacctctag gacagcccaa 2760
aaacgctgtg ccggaagctc ccagggcgac aatgaccatc cttagctgca gctgaccag 2820
ccctaagcac agactttcag accattttgg actaa 2855

```

```

<210> 12
<211> 1152
<212> PRT
<213> Homo sapiens

```

<400> 12

```

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ala Leu Leu Arg Ser
1          5          10          15

```

```

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20          25          30

```

```

Pro Glu Gly Arg Arg Leu Val Gln Pro Gly Asp Pro Ala Ala Phe Arg
35          40          45

```

```

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Gly Ala Arg Pro
50          55          60

```

```

Pro Pro Ala Ala Pro Ser Phe His Gln Val Ser Ser Leu Lys Glu Leu
65          70          75          80

```

```

Val Ala Arg Val Val Gln Arg Leu Cys Glu Arg Gly Glu Arg Asn Val
85          90          95

```

```

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100          105          110

```

```

Met Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115          120          125

```

```

Glu Thr Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130          135          140

```

086,002 - SeqList.ST25.txt

Gly Asp Asp Leu Leu Val His Leu Leu Ala Arg Cys Ala Leu Tyr Leu  
 145 150 155 160  
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 165 170 175  
 Gln Ile Gly Ala Thr Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180 185 190  
 Arg Pro Arg Arg Pro Val Gly Arg Asn Phe Thr Asn Leu Gly Phe Cys  
 195 200 205  
 Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly  
 210 215 220  
 Leu Pro Ser Pro Gly Ala Lys Arg Arg Gly Gly Ser Ala Ser Arg Ser  
 225 230 235 240  
 Leu Pro Leu Pro Lys Lys Ala Arg Arg Gly Ala Ala Pro Glu Pro Glu  
 245 250 255  
 Arg Thr Pro Val Gly Gln Gly Ser Trp Thr Pro Ser Gly Arg Thr Arg  
 260 265 270  
 Val Pro Ser Asp Ala Gly Ser Pro Val Val Ser Pro Ala Arg Pro Ala  
 275 280 285  
 Glu Glu Asp Leu Ser Ser Lys Gly Lys Val Ser Asp Leu Ser Leu Ser  
 290 295 300  
 Gly Ser Val Cys Cys Lys His Lys Pro Ser Ser Pro Pro Ser Leu Ser  
 305 310 315 320  
 Ser Pro Pro Arg Pro Asn Ala Phe Gln Leu Arg Pro Val Tyr Ala Glu  
 325 330 335  
 Thr Lys His Phe Leu Tyr Ser Ser Gly Gly Arg Glu Arg Leu Arg Pro  
 340 345 350  
 Ser Phe Leu Leu Ser Asn Leu Gln Pro Ser Leu Thr Gly Ala Arg Arg  
 355 360 365  
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Thr Ser Gly Pro  
 370 375 380  
 Leu Cys Arg Thr His Arg Leu Ser Arg Arg Tyr Trp Gln Met Arg Pro  
 385 390 395 400



086,002 - SeqList.ST25.txt

Leu Phe Gln Glu Leu Leu Gly Asn His Ala Arg Cys Pro Tyr Val Arg  
 405 410 415  
 Leu Leu Arg Ser His Cys Pro Leu Arg Ala Ala Ala Thr Pro Val Ala  
 420 425 430  
 Gly Ala Leu Asn Thr Ser Pro Pro Gln Gly Ser Val Ala Ala Pro Glu  
 435 440 445  
 Glu Val Ala Ala Pro Gln Glu Gln Thr Asp Ser Thr Arg Leu Met Gln  
 450 455 460  
 Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Leu Arg  
 465 470 475 480  
 Ala Cys Leu Cys Lys Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His  
 485 490 495  
 Asn Glu Arg Arg Phe Leu Lys Asn Val Lys Lys Phe Ile Ser Leu Gly  
 500 505 510  
 Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Lys Val  
 515 520 525  
 Arg Asp Cys Ala Trp Leu Arg Ser Ser Pro Gly Tyr Glu Ser Val Pro  
 530 535 540  
 Ala Ala Glu His Arg Leu Arg Glu Arg Ile Leu Ala Lys Glu His Pro  
 545 550 555 560  
 Phe Leu Phe Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser  
 565 570 575  
 Phe Phe Tyr Ile Thr Glu Ser Thr Phe Gln Lys Asn Arg Leu Phe Phe  
 580 585 590  
 Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Val Arg Gln  
 595 600 605  
 His Leu Glu Arg Val Arg Leu Arg Glu Leu Ser Gln Glu Glu Val Arg  
 610 615 620  
 Gln His Gln Glu Ala Trp Pro Ala Met Pro Ile Cys Arg Leu Arg Phe  
 625 630 635 640  
 Ile Pro Lys Pro Asn Gly Leu Arg Pro Ile Val Asn Met Ser Tyr Ser  
 645 650 655

086,002 - SeqList.ST25.txt

Met Gly Thr Arg Ala Phe Gly Arg Arg Lys Gln Ala Gln His Phe Thr  
660 665 670

Gln Arg Leu Lys Thr Leu Phe Ser Val Leu Asn Tyr Glu Arg Thr Lys  
675 680 685

His Pro His Leu Leu Gly Ala Ser Val Leu Gly Met Asn Asp Ile Tyr  
690 695 700

Arg Thr Trp Arg Thr Phe Val Leu Arg Val Arg Ala Leu Asp Pro Thr  
705 710 715 720

Pro Arg Met Tyr Phe Val Lys Ala Asp Val Thr Gly Ala Tyr Asp Ala  
725 730 735

Ile Pro Gln Asp Lys Leu Val Glu Val Ile Ala Asn Met Ile Arg His  
740 745 750

Ser Glu Ser Thr Tyr Cys Ile Arg Gln Tyr Ala Val Val Gln Arg Asp  
755 760 765

Ala Gln Gly Gln Val His Lys Ser Phe Arg Arg Gln Val Ser Thr Leu  
770 775 780

Ser Asp Leu Gln Pro Tyr Met Gly Gln Phe Leu Lys His Leu Gln Asp  
785 790 795 800

Ser Asp Ala Ser Ala Leu Arg Asn Ser Val Val Ile Glu Gln Ser Ile  
805 810 815

Ser Leu Asn Glu Ala Ser Ser Ser Leu Phe Asp Phe Phe Leu Arg Phe  
820 825 830

Leu Arg His Ser Val Val Lys Ile Gly Gly Arg Cys Tyr Val Gln Cys  
835 840 845

Gln Gly Ile Pro Gln Gly Ser Ser Leu Ser Thr Leu Leu Cys Ser Leu  
850 855 860

Cys Phe Gly Asp Met Glu Asn Lys Leu Phe Ala Glu Val Gln Arg Asp  
865 870 875 880

Gly Leu Leu Leu Arg Phe Val Asp Asp Phe Leu Leu Val Thr Pro His  
885 890 895

Leu Asp Gln Ala Lys Thr Phe Leu Ser Thr Leu Val Arg Gly Val Pro

900

Glu Tyr Gly Cys Met Ile Asn Leu Gln Lys Thr Val Val Asn Phe Pro  
915 920 925

Val Glu Pro Gly Thr Leu Gly Gly Thr Ala Pro Tyr Gln Leu Pro Ala  
930 935 940

His Cys Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Gln Thr Leu  
945 950 955 960

Glu Val Phe Cys Asp Tyr Ser Gly Tyr Ala Arg Thr Ser Ile Lys Ala  
965 970 975

Ser Leu Thr Phe Gln Arg Val Phe Lys Ala Gly Lys Asn Met Arg Asn  
980 985 990

Lys Leu Leu Ser Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp  
995 1000 1005

Leu Gln Val Asn Ser Leu Gln Thr Val Cys Ile Asn Ile Tyr Lys  
1010 1015 1020

Ile Phe Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Ile Gln  
1025 1030 1035

Leu Pro Phe Asp Gln Arg Val Arg Lys Asn Pro Thr Phe Phe Leu  
1040 1045 1050

Gly Ile Ile Ser Ser Gln Ala Ser Cys Cys Tyr Ala Ile Leu Lys  
1055 1060 1065

Val Lys Asn Ala Gly Met Thr Leu Lys Ala Lys Gly Ala Ala Gly  
1070 1075 1080

Ser Phe Pro Pro Glu Ala Ala His Trp Leu Cys Tyr Gln Ala Phe  
1085 1090 1095

Leu Leu Lys Leu Ala Ala His Ser Val Thr Tyr Lys Cys Leu Leu  
1100 1105 1110

Gly Pro Leu Arg Thr Ala Gln Lys Gln Leu Cys Arg Lys Leu Pro  
1115 1120 1125

Glu Ala Thr Met Thr Ile Leu Glu Ala Ala Ala Asp Pro Ala Leu  
1130 1135 1140

086,002 - SeqList.ST25.txt  
Ser Thr Asp Phe Gln Thr Ile Leu Asp  
1145 1150